

1	GACGCGGCTGGCACTGGGTGGGCGCCACACGCTCGGCCACAACCTCCCGGGGCTTCGGCG	60
1	R G W H W V G A H T L G H N S R G F G V	20
61	TGGCCATAGTGGGCAACTACACCGCGGCGCTGCCCACCGAGGCCGCTCTGCGCACGGTGC	120
21	A I V G N Y T A A L P T E A A L R T V R	40
121	GCGACACGCTCCCGAGTTGTGCGGTGCGCGCGGCTCCTGCGGCCAGACTACGCGCTGC	180
41	D T L P S C A V R A G L L R P D Y A L L	60
181	TGGCCACCGCCAGCTGGTGGCACCAGACTGCCCCGGCGACGCGCTCTTCGACCTGCTGC	240
61	G H R Q L V R T D C P G D A L F D L L R	80
241	GCACCTGGCCGCACTTCACCGCGGTGAGTCTTCGCAGCCTGCACTACACGGCCCGCCGCC	300
81	T W P H F T A V S L R S L H Y T A R R P	100
301	CCTCCGTCTACACAAGCTCCACGAGGCCCTGCCCCCTGCCTGTAACAGCTGTGCCCGCA	360
101	S V Y T S S T R P L P P A C N S C A R T	120
361	CAGCCTCAGCCAGGCCCCCAACTTCCCGGCGGCACGTCTATTGAGAACTAGGCCAG	420
121	A S A R P P T S R R H V Y S G N L G P A	140
421	CCTTTGCGGGTCACTCTGCGGGAACATCCCTGATCCTGTGACTTCTGCCTATGCAGCCT	480
141	F A G H S A G N I P D P V T S A Y A A S	160
481	CAGCTCAGCCCCAGACCCAGCCAGCCTGTCCTTTCCCCAGCTCCTAATACCTCTACCTTT	540
161	A Q P Q T Q P A C P F P S S	174
541	CCAGCCAAGGCATGGACCCTGACACCTGCCAACAGCCCCTCTGCCCTCACAACTCAGCC	600
601	TGCCTTCATGACTTCTCTACCCAAGTCACAACCTGTCAGGCTGCACCACCTCATCCTGG	660
661	CCCGCCGAACCTTGACCTCACCCTGCCCCTACCGAAGGCTCTCTGTCCACACAACATG	720

FIG. 1A

721 AACCTAGGCTGTGACCTTTTGCCTTCACAACCTCTGTCCAGTCCTTAATCCTGTGTTGCA 780
781 ATTCTCTGTCCAGACAATCTCAACTCTGAGGTTGCTTGTTTCGTCCCTGACTCCTTAACC 840
841 CCTGATGACAACTCTTATGCCAGCACAACTTTGACCTGATGACCTCATCCCAGCCCTTGA 900
901 TCGCCATCACTAAAACAATTTTAGAATCACACCTGGACAATCTCGTGCTACCTACATACT 960
961 GCCACTCCATTTCATTAAGCTATTGACTAGCACATCCATCTCGGCCTATAGTTGGCTTTG 1020
1021 TCCTCACTCTCTCACTTTGGGCCACTGTCCCCTCCCTGATAAAGGGGATATCACCACCGA 1080
1081 TCCCACAGAAATACAACTACCATCAGAGAATACTATAAACACCTCTATGCAAATAAACT 1140
1041 AGAAAATCTAGAAGAAATGGATAAATTCCTCAACACCCCACTACCAAAAAAAAAAAAAAAAAA 1200

FIG. 1B

1	GCCGTTATGTGAGGTAAGCAGCTTTCTCCAACAGAAGTTCCTCTCTCCTCAAAGGCCAG	60
61	AGTGTCCAGGCCAACCAACTGACCAAGAATTACAACCTGCTGAACTGGCCTCCGAGGTTC	120
121	TCTGCTGGGTCTGTGCCCTGGAAGTGGAGACCCACCATGAAGGCCTGGGGTGCCCTCTGG	180
1	M K A W G A L W	8
181	ATCGTGCTTGATTGCTGCTGTGGCCAGAGCCAGGGGCAGCCTCCTCCTTGCCCTCTGCTC	240
9	I V L G L L L W P E P G A A S S L P L L	28
241	ATGGACTCCATCATCCAGGCCCTTGCTGAACTTGAGCAAAAGGTACCAGTGAAGGCC	300
29	M D S I I Q A L A E L E Q K V P V T E A	48
301	AGCATCACTGCCTCTGCATGGATTCTGTGAGCCAGCAAGTCCAGCACCCACAATTCCTT	360
49	S I T A S A W I L S A K N S S T H N S L	68
361	CACCAGCGCTTGCTGCTGAAGGCACCAAGCCACAACACTACAGAGCCAGATCCTCACTCT	420
69	H Q R L L L K A P S H N T T E P D P H S	88
421	CTCAGCCCCGAGCTTCAAGCACTGATTTCTGAGGTGGCTCAACACGATGTACAGAATGGG	480
89	L S P E L Q A L I S E V A Q H D V Q N G	108
481	CGGGAATATGGAGTGGTGTGGCACCTGATGGCTCCACCGTAGCTGTGAAGCCTCTGCTG	540
109	R E Y G V V L A P D G S T V A V K P L L	128
541	TTTGGGCTAGAGGCCGTCTACAGGCACACAGCGTTGCTAACTTGCCCTTACATTGTCTG	600
129	F G L E A G L Q A H S V A N L P S D C L	148
601	GCTATCCCCTGTGATACTGGAGACACCTTGGCCAATATTAGAGCCACCTGGCCAGGACTC	660
149	A I P C D T G D T L A N I R A T W P G L	168
661	ATGGATGCTTTTCCAAATGCCTCTTCTCCAGATGTTGGAGCCACTTTACCAAACGACAAA	720
169	M D A F P N A S S P D V G A T L P N D K	188

FIG. 2A

721	GCCAAGACTCCCACCACTGTGGACAGACTCCTGGCAATCACCTTGGCTGGTGA	780
189	A K T P T T V D R L L A I T L A G D L G	208
781	CTGACCTTCCTCCACAGGTCCCAGACTTGGAGTCCTCCAGGACTGGGA	840
209	L T F L H R S Q T W S P P G L G T E G C	228
841	TGGGACCAGCTTACTGCCCCAGGGTCTTCACACTGTTGGACCCCCAGGCATCCAGGCTC	900
229	W D Q L T A P R V F T L L D P Q A S R L	248
901	ACCATGGCTTTCCTCAATGGTGCCTTAGATGGAGCTCTCCTTGGGAACCACTTGAGCCAA	960
249	T M A F L N G A L D G A L L G N H L S Q	268
961	ATCCCTAGGCCCCACCCACCCCTCAGCCACCTGCTAAGAGAGTACTATGGAGCTGGGGTG	1020
269	I P R P H P P L S H L L R E Y Y G A G V	288
1021	AATGGAGATCCGGTGTTCGGAAGTAACTTCCGAAGGCAGAACGGTGCTGCTTTGACTTCA	1080
289	N G D P V F R S N F R R Q N G A A L T S	308
1081	GCCCCTACCCTGGCCCAGCAGGTATGGGAGGCCCTTGTCTGTACAGAACTGGAGCCA	1140
309	A P T L A Q Q V W E A L V L L Q K L E P	328
1141	GAACACCTACAGTTGCAGAACATTAGCCAAGAGCAGCTGGCTCAGGTAGCCACCTTGGCT	1200
329	E H L Q L Q N I S Q E Q L A Q V A T L A	348
1201	ACCAAGGAGTTCAGTGGGCTTTCCTGGGATGCCAGCCATTACCCCCGCTGCCGTTGG	1260
349	T K E F T E A F L G C P A I H P R C R W	368
1261	GGAGCGGCTCCCTACCGAGGCCACCCAACACCACTCCGGCTGCCACTTGGATTCTTATAT	1320
369	G A A P Y R G H P T P L R L P L G F L Y	388
1321	GTGCATCACACATACGTGCCAGCGCCACCCTGCACCACCTTCCAGAGCTGCGCCGCCGAT	1380
389	V H H T Y V P A P P C T T F Q S C A A D	408

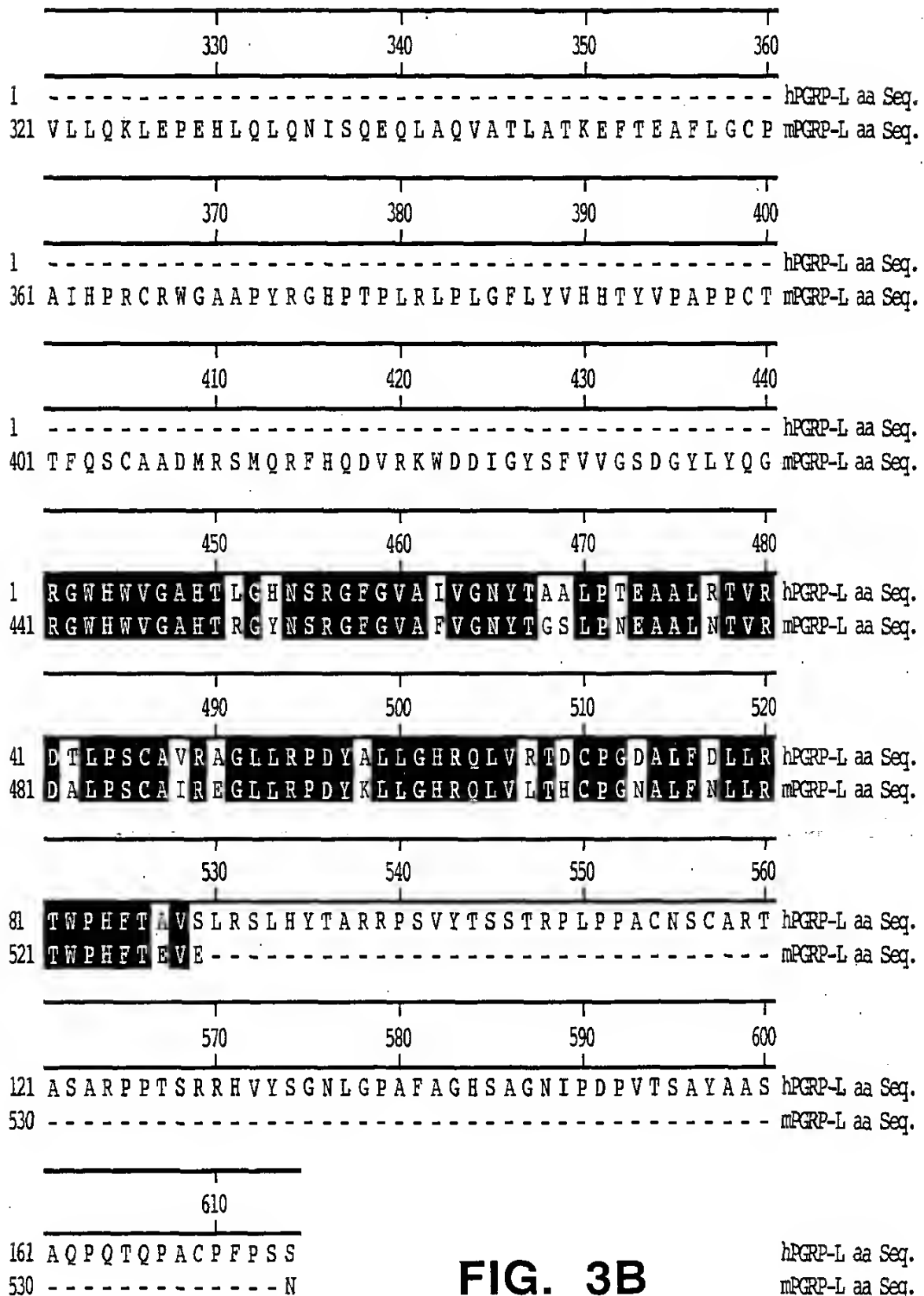
FIG. 2B

1381 ATGCGCTCCATGCAGCGTTTCCACCAGGATGTGCGCAAGTGGGATGACATCGGCTACAGT 1440
 409 M R S M Q R F H Q D V R K W D D I G Y S 428
 1441 TTCGTGGTAGGCTCCGACGGCTATCTGTACCAGGGCCGTGGCTGGCACTGGGTAGGTGCG 1500
 429 F V V G S D G Y L Y Q G R G W H W V G A 448
 1501 CACACACGCGGCTACAACCTCCCGCGGCTTCGGTGTGGCCTTCGTGGGCAACTACACTGGG 1560
 449 H T R G Y N S R G F G V A F V G N Y T G 468
 1561 TCACTGCCCCAACGAAGCTGCGCTGAACACGGTGCGCGACGCGCTCCCGAGCTGCGCAATT 1620
 469 S L P N E A A L N T V R D A L P S C A I 488
 1621 CGCGAAGGTCTCTTGCGGCCAGACTACAAGCTGCTTGCCACCGCCAGCTAGTGCTCACC 1680
 489 R E G L L R P D Y K L L G H R Q L V L T 508
 1681 CACTGCCCCGGGAACGCGCTCTTCAACTTGCTGCGCACCTGGCCTCACTTCACAGAGGTT 1740
 509 H C P G N A L F N L L R T W P H F T E V 528
 1741 GAAAACTAAGAACTCCTTTGAGAGACCCTTGAAGATCCAGGAGGTATTATCCCTGATGAT 1800
 529 E N * 531
 1801 CCTTTGAGCAACCACAGACCTCCAATAAAGGGACCACTGAAAGGAAAAAAAAAAAAAAAA 1860
 1861 AAAAAAAAAAAAAAAAAA 1876

FIG. 2C

		10	20	30	40	
1	-----					hPGRP-L aa Seq.
1	M K A W G A L W I V L G L L L W P E P G A A S S L P L L M D S I I Q A L A E L E					mPGRP-L aa Seq.
		50	60	70	80	
1	-----					hPGRP-L aa Seq.
41	Q K V P V T E A S I T A S A W I L S A K N S S T H N S L H Q R L L L K A P S H N					mPGRP-L aa Seq.
		90	100	110	120	
1	-----					hPGRP-L aa Seq.
81	T T E P D P H S L S P E L Q A L I S E V A Q H D V Q N G R E Y G V V L A P D G S					mPGRP-L aa Seq.
		130	140	150	160	
1	-----					hPGRP-L aa Seq.
121	T V A V K P L L F G L E A G L Q A H S V A N L P S D C L A I P C D T G D T L A N					mPGRP-L aa Seq.
		170	180	190	200	
1	-----					hPGRP-L aa Seq.
161	I R A T W P G L M D A F P N A S S P D V G A T L P N D K A K T P T T V D R L L A					mPGRP-L aa Seq.
		210	220	230	240	
1	-----					hPGRP-L aa Seq.
201	I T L A G D L G L T F L H R S Q T W S P P G L G T E G C W D Q L T A P R V F T L					mPGRP-L aa Seq.
		250	260	270	280	
1	-----					hPGRP-L aa Seq.
241	L D P Q A S R L T M A F L N G A L D G A L L G N H L S Q I P R P H P P L S H L L					mPGRP-L aa Seq.
		290	300	310	320	
1	-----					hPGRP-L aa Seq.
281	R E Y Y G A G V N G D P V F R S N F R R Q N G A A L T S A P T L A Q Q V W E A L					mPGRP-L aa Seq.

FIG. 3A



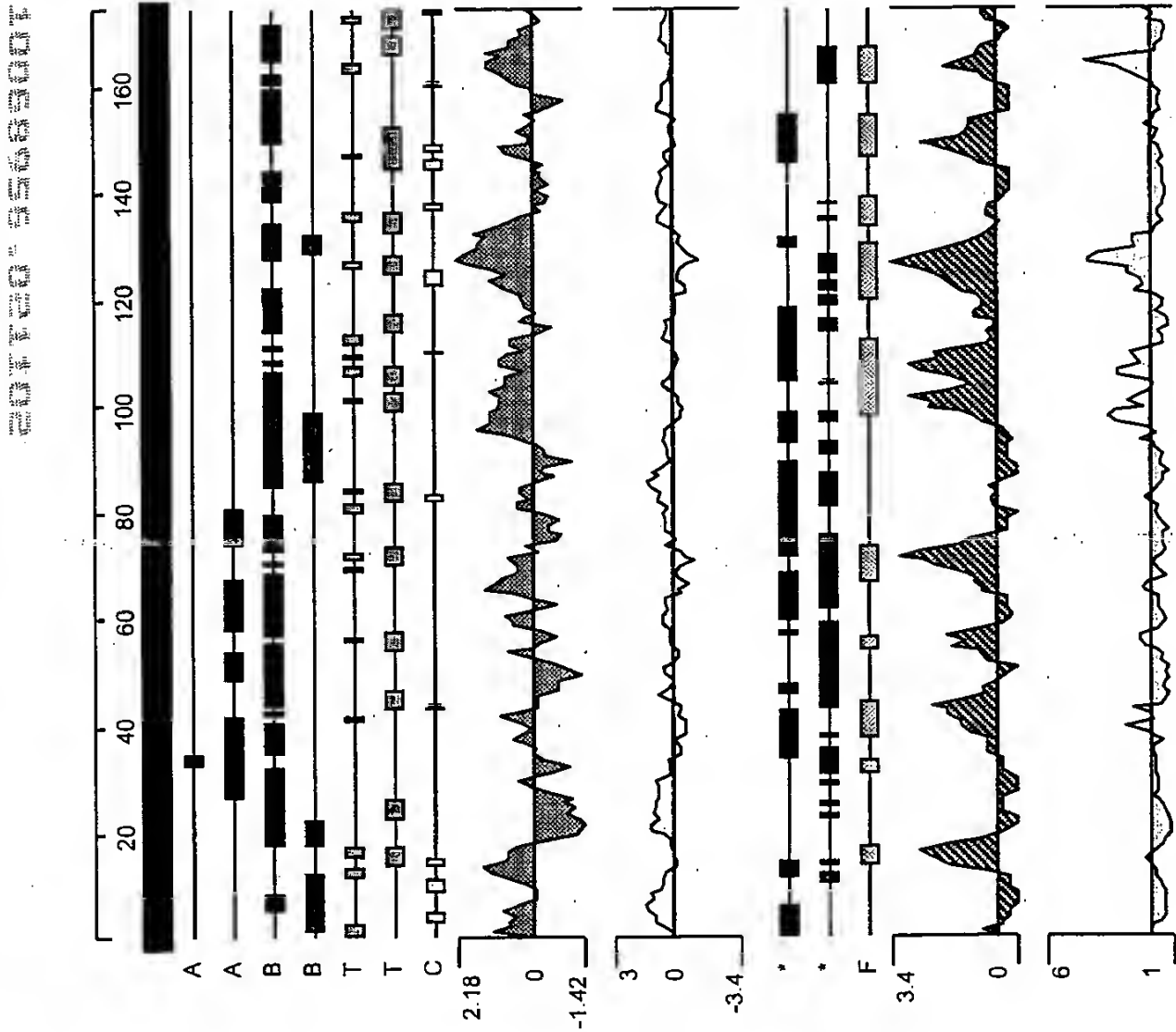


FIG. 4

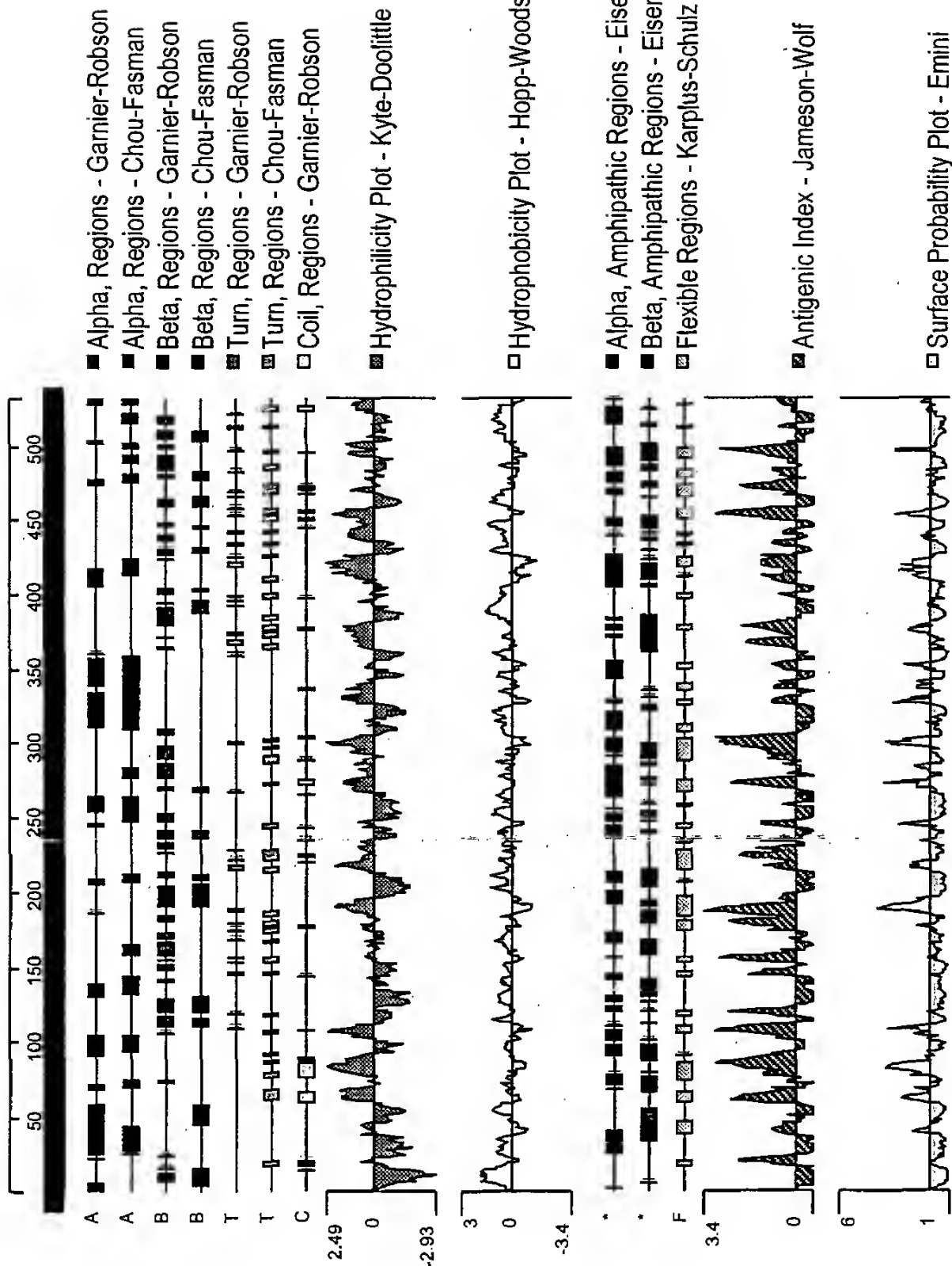


FIG. 5